Remarks

Claims 1-22 are pending in the subject application. By this Supplemental Preliminary Amendment, the applicants have amended claims 1, 3-6, 9, 10, and 22 to correct a minor typographical error. Entry and consideration of the amendment presented herein is respectfully requested. Accordingly, claims 1-22 are currently before the Examiner. Favorable consideration of the pending claims is respectfully requested.

By this Supplemental Preliminary Amendment, the applicants have amended claims 1, 3-6, 9, 10, and 22 to add the recitation *tatD*, which was inadvertently omitted from the independent claims. Support for these amendments can be found, for example, at page 9, lines 10-13, and the dependent claims that recite SEQ ID NO. 14, which is the amino acid sequence encoded by the *tatD* gene. The applicants respectfully submit that these amendments do not constitute new matter.

The applicants believe that the pending claims are in condition for allowance. Such action is respectfully requested.

The Commissioner is hereby authorized to charge any fees under 37 CFR §§1.16 or 1.17 as required by this paper to Deposit Account No. 19-0065.

The applicants invite the Examiner to call the undersigned if clarification is needed on any of this Amendment, or if the Examiner believes a telephonic interview would expedite the prosecution of the subject application to completion.

Respectfully submitted,

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GPL/sl
Attachment: Marked-Up Version of Amended Claims

Docket No. GJE-65
Serial No. 09/830,807

Marked-Up Version of Amended Claims

Claim 1 (twice amended):

1. An isolated peptide encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 3 (twice amended):

3. An isolated polynucleotide which comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 4 (twice amended):

4. A host transformed to express a peptide encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 5 (twice amended):

5. A vaccine comprising a peptide, or the means for its expression, wherein said peptide is encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eckl*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said

homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 6 (twice amended):

6. A vaccine comprising a microorganism having a virulence gene mutation, wherein the gene is selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eck1*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 9 (twice amended):

9. A method for screening potential drugs, or for the detection of virulence, wherein said method utilizes a peptide encoded by an operon, wherein said operon comprises a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eck1*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 10 (twice amended):

10. A method for treatment or prevention of a condition associated with infection by a Gram-negative bacterium, said method comprising administering a vaccine to a person or animal in need thereof, wherein said vaccine comprises a peptide, or a host transformed to express said peptide, wherein said peptide is encoded by an operon comprising a gene selected from the group consisting of *tatA*, *tatB*, *tatD*, *tatC*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eck1*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.

Claim 22 (amended):

22. A method for treatment or prevention of a condition associated with infection by a Gram-negative bacterium, said method comprising administering a nucleotide to a person or animal in need thereof, wherein said nucleotide comprises an operon including a gene selected from the group consisting of *tatA*, *tatB*, *tatC*, *tatD*, *tatE*, *mdoG*, *creC*, *recG*, *yggN*, *eck1*, *iroD*, *iroC*, *iroE*, *mtd2*, and *ms1* to *ms16*, obtainable from *E. coli* K1, or a homologue thereof in a Gram-negative bacterium, wherein said homologue has at least 30% homology at the amino acid or nucleotide level, or a functional fragment thereof.